



## MISSION

*The NCI Clinical Proteomic Technologies Initiative for Cancer seeks to foster the building of an integrated foundation of proteomic technologies, data, reagents and reference materials, and analysis systems to systematically advance the application of protein science to accelerate discovery and clinical research in cancer.*

## NCI CLINICAL PROTEOMIC TECHNOLOGIES INITIATIVE FOR CANCER

The NCI Clinical Proteomic Technologies Initiative for Cancer (CPTI) represents a highly organized approach to assess and apply proteomic technologies and data resources to solve critical problems in cancer research.

Proteins are of major scientific interest to cancer researchers, as they play an important role in supporting cell structure and function, in carrying signals within and among cells, and in regulating the level of biological activity. Therefore, it is critical to accurately measure select proteins that may have great potential as clinical diagnostic tools for the early detection of cancer. These proteins may also have application in the development of molecular imaging tools to monitor clinical outcomes, in the discovery of targeted drugs, and in the guidance of clinical trials.

The development of accurate, reliable, and standardized protein measurement technologies is a complex challenge, requiring a large-scale, coordinated effort among multiple laboratories linked by powerful informatics capabilities. Current proteomic methodologies have not sufficiently addressed either the lack of reproducibility of data from measurements made on different technology platforms, nor the obstacles in handling complex biological mixtures with the broad variability of protein concentrations that are typical of clinical specimens.

## BENEFITS OF THE INITIATIVE

Through interactions with existing NCI resources and other federal and private sector groups, CPTI is expected to catalyze targeted discovery and development efforts and foster new partnerships with the private sector. These interactions and partnerships will help overcome the obstacles to recent attempts at applying protein measurement technology – including mass spectrometry and affinity-based detection methods – to clinical applications.

CPTI will harness the team efforts necessary to establish standards, ensure rigorous quality control measures, and develop an informatics platform capable of aggregating and comparing data across laboratories to support and enable new approaches to protein and peptide-based discovery of biomarkers for cancer processes.

## NCI PROGRAM INTEGRATION

CPTI works in partnership with existing NCI resources, including caBIG™ (see sidebar) and the Early Detection Research Network (EDRN), to create a national proteomics research infrastructure. The Initiative will complement existing NCI endeavors in structural and functional proteomics, including the Biomedical and Clinical Proteomics Programs, to maximize the impact of its findings. Support from this Initiative will be provided to NCI-designated Cancer Centers dedicated to biomarker discovery at a particular cancer site (e.g., breast, lung, prostate, or colon). In addition, the CPTI will integrate with Specialized Programs of Research Excellence (SPORes) to help move basic research findings from the laboratory to clinical settings.

## ADVANCING THE FIELD OF CANCER PROTEOMICS

In order to improve proteomic analysis platforms – and thereby reliably identify, quantify, and compare proteins and peptides in complex biological mixtures and across diverse analysis platforms and instruments – the CPTI is designed to:

- Build an integrative team framework that networks multiple research laboratories to permit large-scale, real-time exchange and application of existing and newly developed protein measurement technologies, biological resources, and data dissemination;
- Refine and optimize technologies, reagents, methods, and analysis platforms that will ensure reliable and reproducible separation, capture, identification, quantification, and validation of protein measurements from complex biological mixtures; and
- Evaluate new technological approaches to separate and recognize proteins of significance to the molecular and cellular events that occur during the process of cancer development.

## COMPONENTS OF THE INITIATIVE

The CPTI is an integrated approach to assess, enhance, and develop proteomic technology measurement capabilities. With input from the international proteomics and cancer research communities, the Initiative has established three major programs:

### *Clinical Proteomic Technology Assessment for Cancer (CPTAC)*

The goal of CPTAC is to improve the ability to rigorously and reproducibly detect, identify, and quantify proteins and peptides of interest in biological specimens by exploring and improving proteomics technologies and by establishing broadly available research reference resources. The CPTAC institutions will serve as a multidisciplinary network for technology and platform development and design rigorous technology assessment, standard protocols, and methods to ensure data reproducibility. The emphasis of this program is on mass spectrometry and affinity capture proteomic analysis platforms.

### *Advanced Proteomic Platforms and Computational Sciences*

The goal of the Advanced Proteomic Platforms and Computational Sciences effort is to advance the technological and analytical capabilities in proteomic research, which will allow the research community to better characterize and understand the differences between the normal and diseased human proteome and to develop diagnostic and treatment procedures based on these distinctions. This effort will support the development of innovative tools and enabling technologies for protein and peptide measurement and support algorithm development and computational methods to interrogate emerging pre-processed data sets.

### *Clinical Proteomic Reagents Resource*

The Clinical Proteomic Reagents Resource will organize tools, reagents, and enabling technologies to support protein and peptide measurement and analysis efforts. The Resource will serve as a central (virtual) source for reagents for the scientific community. The Resource will develop standard reagents, perform characterization, provide an interactive resource catalog through the cancer Biomedical Informatics Grid™ (caBIG™), and expedite acquisition and distribution of reagents and data on reagent performance.

### caBIG™

The cancer Biomedical Informatics Grid™ (caBIG™) is an information network enabling the cancer community to share data and knowledge to accelerate the discovery of new approaches to detection, diagnosis, treatment, and prevention of cancer, and to improve patient outcomes. caBIG™ connects scientists and practitioners through a shareable, interoperable infrastructure; and builds or adapts tools for collecting, analyzing, integrating, and disseminating information associated with cancer research and care.

The NCI Clinical Proteomic Technologies Initiative for Cancer is working closely with caBIG™ to assure that computational platforms developed for the program are caBIG™ compatible.

Platforms currently being made compatible include CPAS and Mass Spectrometry data converters, in addition to all future proteomic informatics tools developed by the Initiative. For additional information about caBIG™, please visit <http://cabig.nci.nih.gov>.

### FOR MORE INFORMATION:

U.S. DEPARTMENT OF HEALTH AND HUMAN  
SERVICES

National Institutes of Health

National Cancer Institute

Office of Technology & Industrial Relations

Building 31, Room 10A49  
31 Center Drive, MSC 2580  
Bethesda, MD 20892-2580

**Phone:** (301) 496-1550

**Fax:** (301) 496-7807

**E-mail:** [cancer.proteomics@mail.nih.gov](mailto:cancer.proteomics@mail.nih.gov)

**Web site:** <http://proteomics.cancer.gov>

